



SEQUENCE LISTING

<110> PEPICELLI, CARMEN V.
LEWIS, PAULA M.
MCMAHON, ANDREW P.

<120> REGULATION OF LUNG TISSUE BY HEDGEHOG-LIKE POLYPEPTIDES,
AND FORMULATIONS AND USES RELATED THERETO

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<140> 09/394,020
<141> 1999-09-10

<150> 60/099,952
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<170> PatentIn Ver. 2.1

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960	agc ggt cag ctt aaa tct gtc atc gtg cag cggtt gtt gat tac acg gag gag Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu 305 310 315 320
1008	cag cgg ggc tcg ttc gca cca gtg act gca cat ggg acc att gtg gtc Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val 325 330 335
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1104	gcg cat ttg gcc ttc gcg ccc gcc agg ctc tat tat tac gtg tca tca Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser 355 360 365
1152	tcc ctg tcc ccc aaa act cca gca gtc ggt cca atg cga ctt tac aac Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn 370 375 380
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ctg gta tgc tcg qga ctg gcg tgc gga ccg ggc agg ggg ttc ggg aag Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys 20 25 30	
96	

agg agg cac ccc aaa aag ctg acc cct tta gcc tac aag cag ctt atc Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile 35 40 45	144
ccc aat gtg gcc gag aag acc cta ggc gcc agc gga agg tat gaa ggg Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly 50 55 60	192
aag atc tcc aga aac tcc gag cga ttt aag gaa ctc acc ccc aat tac Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr 65 70 75 80	240
aac ccc gac atc ata ttt aag gat gaa gaa aac acc gga gcg gac agg Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg 85 90 95	288
ctg atg act cag agg tgt aag gac aag ttg aac gct ttg gcc atc tcg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser 100 105 110	336
gtg atg aac cag tgg cca gga gtg aaa ctg cgg gtg acc gag ggc tgg Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp 115 120 125	384
gac gaa gat ggc cac cac tca gag gag tct ctg cac tac gag ggc cgc Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg 130 135 140	432
gca gtg gac atc acc acg tct gac cgc gac cgc agc aag tac ggc atg Ala Val Asp Ile Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met 145 150 155 160	480
ctg gcc cgc ctg gcg gtg gag ggc ttc gac tgg gtg tac tac gag Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu 165 170 175	528
tcc aag gca cat atc cac tgc tcg gtg aaa gca gag aac tcg gtg gcg Ser Lys Ala Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala 180 185 190	576
gcc aaa tcg gga ggc tgc ttc ccg ggc tcg gcc acg gtg cac ctg gag Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu 195 200 205	624
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Thr	Arg	Glu	Pro	Arg	Glu	Arg	Leu	Leu	Leu	Thr	Ala	Ala	His	Leu	Leu				
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ttt	gt	g	cg	ccg	cac	aac	gac	tcg	gcc	acc	ggg	gag	ccc	gag	g	cg	tcc	864	
Phe	Val	Ala	Pro	His	Asn	Asp	Ser	Ala	Thr	Gly	Glu	Pro	Glu	Ala	Ser				
275							280							285					
tcg	ggc	tcg	ggg	ccg	cct	tcc	ggg	ggc	gca	ctg	ggg	cct	cg	g	cg	ctg	912		
Ser	Gly	Ser	Gly	Pro	Pro	Ser	Gly	Gly	Ala	Leu	Gly	Pro	Arg	Ala	Leu				
290							295							300					
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Phe	Ala	Ser	Arg	Val	Arg	Pro	Gly	Gln	Arg	Val	Tyr	Val	Val	Ala	Glu				
305							310					315					320		
cgt	gac	ggg	gac	cgc	cg	cc	tc	ctg	ccc	gcc	g	c	gt	cac	agc	gt	tg	acc	1008
Arg	Asp	Gly	Asp	Arg	Arg	Leu	Leu	Pro	Ala	Ala	Val	His	Ser	Val	Thr				
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cta	agc	gag	gag	ggc	g	ccg	ggc	g	cc	tac	g	c	g	cc	c	ag	ggc	1056	
Leu	Ser	Glu	Glu	Ala	Ala	Gly	Ala	Tyr	Ala	Pro	Leu	Thr	Ala	Gln	Gly				
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acc	att	ctc	atc	aac	cgg	gt	tg	gc	tc	tg	tac	gc	g	tc	atc	g	ag	1104	
Thr	Ile	Leu	Ile	Asn	Arg	Val	Leu	Ala	Ser	Cys	Tyr	Ala	Val	Ile	Glu				
355							360							365					
gag	cac	agc	tgg	g	cg	cac	cg	gg	cc	ttc	g	cc	ttc	cg	ct	g	cg	cac	1152
Glu	His	Ser	Trp	Ala	His	Arg	Ala	Phe	Ala	Pro	Phe	Arg	Leu	Ala	His				
370							375							380					
g	cg	ct	ctg	g	ca	ctg	g	cg	cc	g	cg	c	g	cc	gg	g	gg	gac	1200
Ala	Leu	Leu	Ala	Ala	Leu	Ala	Pro	Ala	Arg	Thr	Asp	Arg	Gly	Gly	Asp				
385							390							395				400	
agc	ggc	ggg	gac	cgc	ggg	ggc	ggc	ggc	ggc	aga	gta	g	cc	ct	acc			1248	
Ser	Gly	Gly	Asp	Arg	Gly	Gly	Gly	Gly	Gly	Gly	Arg	Val	Ala	Leu	Thr				
405							410							415					
g	ct	cca	gg	gt	gt	g	cc	g	ct	gg	g	gg	cc	ac	g	cg	gg	atc	1296
Ala	Pro	Gly	Ala	Ala	Asp	Ala	Pro	Gly	Ala	Gly	Ala	Thr	Ala	Gly	Ile				
420							425							430					
cac	tgg	ta	tc	c	tg	ct	tc	ta	ca	at	gg	ac	tgg	ct	ct	g	ac	1344	
His	Trp	Tyr	Ser	Gln	Leu	Leu	Tyr	Gln	Ile	Gly	Thr	Trp	Leu	Leu	Asp				
435							440							445					
agc	gag	gg	ct	ca	cc	ct	gg	gc	at	g	cg	gt	tc	a	g	cc	nn	agc	1392
Ser	Glu	Ala	Leu	His	Pro	Leu	Gly	Met	Ala	Val	Lys	Ser	Ser	Xaa	Ser				
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cgg	ggg	gg	1425																
Arg	Gly	Ala	Gly	Gly	Ala	Arg	Gly	Ala	Arg	Glu	Gly	Ala							
465							470							475					

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Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser Glu His	
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tcg gcc gca gcc aag acg ggc ggc tgc ttc cct gcc gga gcc cag gta	680
Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala Gln Val	
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200	205
205	210
cgc ctg gag agt ggg gcg cgt gtg gcc ttg tca gcc gtg agg ccg gga	728
Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg Pro Gly	
215	220
220	225
gac cgt gtg ctg gcc atg ggg gag gat ggg agc ccc acc ttc agc gat	776
Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe Ser Asp	
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235	240
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Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala Phe Gln	
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Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr Pro Ala	
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265	270
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His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala Arg Phe	
275	280
280	285
285	290
cgg gcc aca ttt gcc agc cac gtg cag cct ggc cag tac gtg ctg gtg	968
Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val Leu Val	
295	300
300	305
gct ggg gtg cca ggc ctg cag cct gcc cgc gtg gca gct gtc tct aca	1016
Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val Ser Thr	
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cac gtg gcc ctc ggg gcc tac gcc ccg ctc aca aag cat ggg aca ctg	1064
His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly Thr Leu	
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Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala Asp His	
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His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His Ser Leu	
355	360
360	365
365	370
gca tgg ggc agc tgg acc ccg ggg gag ggt gtg cat tgg tac ccc cag	1208
Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr Pro Gln	
375	380
380	385
ctg ctc tac cgc ctg ggg cgt ctc ctg cta gaa gag ggc agc ttc cac	1256
Leu Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Gly Ser Phe His	
390	395
395	400

cca ctg ggc atg tcc ggg gca ggg agc tgaaaggact ccaccgctgc 1303
 Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

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 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
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 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45

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 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

ggg agg gtg gca agg ggc tcc gag cgc ttc cgg gac ctc gtg ccc aac 240
 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

tac aac ccc gac atc atc ttc aag gat gag gag aac agt gga gcc gac 288
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

cgc ctg atg acc gag cgt tgc aag gag agg gtg aac gct ttg gcc att 336
 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

gcc gtg atg aac atg tgg ccc gga gtg cgc cta cga gtg act gag ggc 384
 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

tgg gac gag gac ggc cac cac gct cag gat tca ctc cac tac gaa ggc Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly 130 135 140	432
cgt gct ttg gac atc act acg tct gac cgc gac cgc aac aag tat ggg Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly 145 150 155 160	480
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gcg gtc cgg gcg ggc ggc tgc ttt ccg gga aat gca act gtg cgc ctg Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu 195 200 205	624
tgg agc ggc gag cgg aaa ggg ctg cgg gaa ctg cac cgc gga gac tgg Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp 210 215 220	672
gtt ttg gcg gcc gat gcg tca ggc cgg gtg gtg ccc acg ccg gtg ctg Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu 225 230 235 240	720
ctc ttc ctg gac cgg gac ttg cag cgc cgg gct tca ttt gtg gct gtg Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val 245 250 255	768
gag acc gag tgg cct cca cgc aaa ctg ttg ctc acg ccc tgg cac ctg Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu 260 265 270	816
gtg ttt gcc gct cga ggg ccg gcg ccc gcg cca ggc gac ttt gca ccg Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro 275 280 285	864
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Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys		
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Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val		
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Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn		
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tca gtg gct gct aaa tca gga gga tgt ttt cct ggg tct ggg acg gtg		624
Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val		
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aca ctt ggt gat ggg acg agg aaa ccc atc aaa gat ctt aaa gtg ggc		672
Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly		
210 215 220		
gac cgg gtt ttg gct gca gac gag aag gga aat gtc tta ata agc gac		720
Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp		
225 230 235 240		
ttt att atg ttt ata gac cac gat ccg aca acg aga agg caa ttc atc		768
Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile		
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Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala		
260 265 270		
cac cta gtt ttc gtt gga aac tct tca gca gct tcg ggt ata aca gca		864
His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala		
275 280 285		
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Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu		
290 295 300		
gac aca tgc gag agc ctc aag agc gtt aca gtg aaa agg att tac act		960
Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr		
305 310 315 320		
gag gag cac gag ggc tct ttt gcg cca gtc acc gcg cac gga acc ata		1008
Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile		
325 330 335		
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Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His		
340 345 350		
aaa tgg gca cat tgg gct ttt gcg ccg gtc agg ttg tgt cac aag ctg		1104
Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu		
355 360 365		

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Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu			
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Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp			
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Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys			
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Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg			
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Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr			
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Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly			
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Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu			
100	105	110	
Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr			
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Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr			
130	135	140	
Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys			
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Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val			
165	170	175	
Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn			
180	185	190	

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
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 His Leu Glu His Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly
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 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
 225 230 235 240
 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
 245 250 255
 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
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 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
 275 280 285
 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
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 Arg Val Tyr Val Leu Gly Glu Gly Gln Gln Leu Leu Pro Ala Ser
 305 310 315 320
 Val His Ser Val Ser Leu Arg Glu Glu Ala Ser Gly Ala Tyr Ala Pro
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 340 345 350
 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365
 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380
 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
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 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
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 Pro Leu Gly Met Val Ala Pro Ala Ser
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Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60

Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
 100 105 110

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
 130 135 140

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
 145 150 155 160

Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175

Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
 180 185 190

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
 195 200 205

Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
 210 215 220

Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
 225 230 235 240

Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
 245 250 255

Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
 260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300

Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
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 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
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 35 40 45
 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60
 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80
 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95
 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110
 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125
 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140
 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160
 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175
 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190
 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
 210 215 220
 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
 225 230 235 240
 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
 245 250 255
 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
 325 330 335
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380
 Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

<210> 13
 <211> 437
 <212> PRT
 <213> Murine sp.

<400> 13
 Met Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15
 Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30
 Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45
 Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60

Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95

Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
 100 105 110

Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
 130 135 140

Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly
 145 150 155 160

Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
 165 170 175

Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val
 180 185 190

Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu
 195 200 205

Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg
 210 215 220

Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu
 225 230 235 240

Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile
 245 250 255

Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu
 260 265 270

Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser
 275 280 285

Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val
 290 295 300

Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser
 305 310 315 320

Val Thr Leu Arg Glu Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala
 325 330 335

His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val
 340 345 350

Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu
 355 360 365

Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly
 370 375 380
 Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly
 385 390 395 400
 Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His
 405 410 415
 Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met
 420 425 430
 Ala Val Lys Ser Ser
 435

<210> 14
 <211> 418
 <212> PRT
 <213> Brachydanio rerio

<400> 14
 Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
 1 5 10 15
 Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
 20 25 30
 Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45
 Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60
 Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80
 Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95
 Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
 100 105 110
 Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125
 Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140
 Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
 145 150 155 160
 Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175
 Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
 195 200 205
 Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
 210 215 220
 Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
 225 230 235 240
 Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
 245 250 255
 Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
 260 265 270
 Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
 275 280 285
 Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
 290 295 300
 Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
 305 310 315 320
 Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
 325 330 335
 Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
 340 345 350
 Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Tyr Val Ser Ser
 355 360 365
 Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
 370 375 380
 Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
 385 390 395 400
 Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
 405 410 415
 Ser Ser

<210> 15
 <211> 475
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Xaa at position 463 is any or unknown amino acid

<400> 15
 Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
 1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
 20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
 35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
 50 55 60

Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
 65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
 85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
 100 105 110

Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
 115 120 125

Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg
 130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met
 145 150 155 160

Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
 165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
 180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu
 195 200 205

Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val
 210 215 220

Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr
 225 230 235 240

Phe Leu Asp Arg Asp Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu
 245 250 255

Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu
 260 265 270

Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser
 275 280 285

Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu
 290 295 300

Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu
 305 310 315 320

Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr
 325 330 335

Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly
 340 345 350

Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu
 355 360 365

Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His
 370 375 380

Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp
 385 390 395 400

Ser Gly Gly Asp Arg Gly Gly Gly Arg Val Ala Leu Thr
 405 410 415

Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile
 420 425 430

His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp
 435 440 445

Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser
 450 455 460

Arg Gly Ala Gly Gly Ala Arg Glu Gly Ala
 465 470 475

<210> 16
 <211> 411
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1 5 10 15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30

Val Val Gly Ser Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205

Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg
 210 215 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe
 225 230 235 240

Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala
 245 250 255

Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270

Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285

Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300

Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320

Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
 325 330 335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350

Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His
 355 360 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr
 370 375 380

Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Gly Ser
 385 390 395 400

Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

<210> 17
<211> 396
<212> PRT
<213> Homo sapiens

<400> 17
Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
1 5 10 15
Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
20 25 30
Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
35 40 45
Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
50 55 60
Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
65 70 75 80
Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
85 90 95
Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
100 105 110
Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125
Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
130 135 140
Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
145 150 155 160
Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
165 170 175
Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
180 185 190
Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
195 200 205
Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
210 215 220
Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
225 230 235 240
Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
245 250 255
Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
 275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
 290 295 300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
 305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
 325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
 340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
 355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
 370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
 385 390 395

<210> 18

<211> 416

<212> PRT

<213> Brachydanio rerio

<400> 18

Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
 1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
 20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
 35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
 50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
 65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
 85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
 100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
 115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
 130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
 145 150 155 160
 Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
 165 170 175
 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
 180 185 190
 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val
 195 200 205
 Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly
 210 215 220
 Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp
 225 230 235 240
 Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile
 245 250 255
 Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala
 260 265 270
 His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala
 275 280 285
 Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu
 290 295 300
 Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr
 305 310 315 320
 Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile
 325 330 335
 Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His
 340 345 350
 Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu
 355 360 365
 Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu
 370 375 380
 Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp
 385 390 395 400
 Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser
 405 410 415

<210> 19
 <211> 1416
 <212> DNA
 <213> Drosophila sp.

<220>
 <221> CDS
 <222> (1)..(1413)

<400> 19
 atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc 48
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15

tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag ttc cag 96
 Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
 20 25 30

ctc caa atc cgc agc gag ctc cat ctc cgc aag ccc gca aga aga acg 144
 Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
 35 40 45

caa acg atg cgc cac att gcg cat acg cag cgt tgc ctc agc agg ctg 192
 Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
 50 55 60

acc tct ctg gtg gcc ctg ctg atc gtc ttg ccg atg gtc ttt agc 240
 Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65 70 75 80

ccg gct cac agc tgc ggt cct ggc cga gga ttg ggt cgt cat agg gcg 288
 Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
 85 90 95

cgc aac ctg tat ccg ctg gtc ctc aag cag aca att ccc aat cta tcc 336
 Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
 100 105 110

gag tac acg aac agc gcc tcc gga cct ctg gag ggt gtg atc cgt cgg 384
 Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
 115 120 125

gat tcg ccc aaa ttc aag gac ctc gtg ccc aac tac aac agg gac atc 432
 Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
 130 135 140

ctt ttc cgt gac gag gaa ggc acc gga gcg gat ggc ttg atg agc aag 480
 Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
 145 150 155 160

cgc tgc aag gag aag cta aac gtg ctg gcc tac tcg gtg atg aac gaa 528
 Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
 165 . 170 175

tgg ccc ggc atc cgg ctg gtc acc gag agc tgg gac gag gac tac 576
 Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
 180 185 190

cat cac ggc cag gag tcg ctc cac tac gag ggc cga gcg gtg acc att 624
 His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
 195 200 205

gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu 210 215 220	672
gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His 225 230 235 240	720
atc tac tgc tcc gtc aag tca gat tcg tcg atc agt tcc cac gtg cac Ile Tyr Cys Ser Val Lys Ser Asp Ser Ile Ser Ser His Val His 245 250 255	768
ggc tgc ttc acg ccg gag agc aca gcg ctg ctg gag agt gga gtc cg Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg 260 265 270	816
aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr 275 280 285	864
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg 290 295 300	912
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly 305 310 315 320	960
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro 325 330 335	1008
gag agc cag aag ctc acg ttt gtg ttt ggc cat cgc atc gag gag aag Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys 340 345 350	1056
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln 355 360 365	1104
cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro 370 375 380	1152
ctg acc cgc gag ggc acc att gtg gtc aac tcg gtg gcc gcc agt tgc Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys 385 390 395 400	1200
tat gcg gtg atc aac agt cag tcg ctg gcc cac tgg gga ctg gct ccc Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro 405 410 415	1248
atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln 420 425 430	1296

ttg cac agt tcg ccg aag gtg gtg agc tcg gcg cag cag cag aat ggc 1344
 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Asn Gly
 435 440 445

atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg 1392
 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460

ccg cag agc tgg cgc cac gat tga 1416
 Pro Gln Ser Trp Arg His Asp
 465 470

<210> 20
 <211> 471
 <212> PRT
 <213> Drosophila sp.

<400> 20
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15

Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln Phe Gln
 20 25 30

Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr
 35 40 45

Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu
 50 55 60

Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser
 65 70 75 80

Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala
 85 90 95

Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser
 100 105 110

Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg
 115 120 125

Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile
 130 135 140

Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys
 145 150 155 160

Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu
 165 170 175

Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr
 180 185 190

His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile
 195 200 205

Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu
 210 215 220

Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His
 225 230 235 240

Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His
 245 250 255

Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg
 260 265 270

Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr
 275 280 285

Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg
 290 295 300

Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly
 305 310 315 320

Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
 325 330 335

Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
 340 345 350

Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
 355 360 365

Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
 370 375 380

Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
 385 390 395 400

Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
 405 410 415

Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
 420 425 430

Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
 435 440 445

Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460

Pro Gln Ser Trp Arg His Asp
 465 470

<210> 21
 <211> 221
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: degenerate
polypeptide sequence

<220>
<221> MOD_RES
<222> (7)
<223> Gly, Ala, Val, Leu, Ile, Phe, Tyr or Trp

<220>
<221> MOD_RES
<222> (9)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (44)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (85)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (93)
<223> Lys, Arg, His, Asn or Gln

<220>
<221> MOD_RES
<222> (98)
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> (112)
<223> Ser, Thr, Tyr, Trp or Phe

<220>
<221> MOD_RES
<222> (132)
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> (137)
<223> Met, Cys, Ser or Thr

<220>
<221> MOD_RES
<222> (139)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (181)
<223> Leu, Val, Met, Thr or Ser

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<220>
<221> MOD_RES
<222> (183)
<223> His, Phe, Tyr, Ser, Thr, Met or Cys

<220>
<221> MOD_RES
<222> (185)
<223> Gln, Asn, Glu, or Asp

<220>
<221> MOD_RES
<222> (186)
<223> His, Phe, Tyr, Thr, Gln, Asn, Glu or Asp

<220>
<221> MOD-RES
<222> (189)
<223> Gln, Asn, Glu, Asp, Thr, Ser, Met or Cys

<220>
<221> MOD_RES
<222> (191)
<223> Ala, Gly, Cys, Leu, Val or Met

<220>
<221> MOD_RES
<222> (196)
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser, Thr or Cys

<220>
<221> MOD_RES
<222> (200)
<223> Arg, Lys, Met or Ile

<220>
<221> MOD_RES
<222> (206)
<223> Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr or Met

<220>
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<222> (207)
<223> Ala, Gly, Cys, Asp, Asn, Glu or Gln

<220>
<221> MOD_RES
<222> (209)
<223> Arg, Lys, Met, Ile, Asn, Asp, Glu or Gln

<220>
<221> MOD_RES
<222> (211)
<223> Leu, Val, Met or Ile

<220>
<221> MOD_RES
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<223> Phe, Tyr, Thr, His or Trp

<220>

<221> MOD_RES

<222> (216)

<223> Ile, Val, Leu or Met

<220>

<221> MOD_RES

<222> (217)

<223> Met, Cys, Ile, Leu, Val, Thr or Ser

<220>

<221> MOD_RES

<222> (219)

<223> Leu, Val, Met, Thr or Ser

<220>

<223> each Xaa may also be any amino acid.

<400> 21

Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu

1

5

10

15

Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu
35 40 45

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
50 55 60

Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
65 70 75 80

Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
85 90 95

Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
100 105 110

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
115 120 125

Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
130 135 140

Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
145 150 155 160

Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe
165 170 175

Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val
180 185 190

Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
195 200 205

Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
210 215 220

<210> 22
<211> 167
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: degenerate
polypeptide sequence

<220>
<221> MOD_RES
<222> (7)
<223> Gly, Ala, Val, Leu, Ile, Pro, Phe or Tyr

<220>
<221> MOD_RES
<222> (8)
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> (9)
<223> Gly, Ala, Val, Leu, Ile, Lys, His or Arg

<220>
<221> MOD_RES
<222> (12)
<223> Lys, Arg or His

<220>
<221> MOD_RES
<222> (13)
<223> Phe, Trp, Tyr or an amino acid gap

<220>
<221> MOD_RES
<222> (14)
<223> Gly, Ala, Val, Leu, Ile or an amino acid gap

<220>
<221> MOD_RES
<222> (17)
<223> Asn, Gln, His, Arg or Lys

<220>
<221> MOD_RES
<222> (19)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES

<222> (22)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (27)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (29)
<223> Ser, Thr, Gln or Asn

<220>
<221> MOD_RES
<222> (30)
<223> Met, Cys, Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (31)
<223> Gly, Ala, Val, Leu, Ile or Pro

<220>
<221> MOD_RES
<222> (33)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (40)
<223> Gly, Ala, Val, Leu, Ile, Pro, Arg, His or Lys

<220>
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<222> (41)
<223> Gly, Ala, Val, Leu, Ile, Phe or Tyr

<220>
<221> MOD_RES
<222> (44)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (45)
<223> Gly, Ala, Val, Leu, Ile, Ser or Thr

<220>
<221> MOD_RES
<222> (46)
<223> Thr or Ser

<220>
<221> MOD_RES
<222> (48)
<223> Gly, Ala, Val, Leu, Ile, Asn or Gln

<220>
<221> MOD_RES
<222> (53)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (54)
<223> Asp or Glu

<220>
<221> MOD_RES
<222> (71)
<223> Ser or Thr

<220>
<221> MOD_RES
<222> (79)
<223> Glu, Asp, Gln or Asn

<220>
<221> MOD_RES
<222> (83)
<223> Glu or Asp

<220>
<221> MOD_RES
<222> (84)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (85)
<223> Gly, Ala, Val, Leu or Ile

<220>
<221> MOD_RES
<222> (87)
<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
<221> MOD_RES
<222> (95)
<223> Met, Cys, Gln, Asn, Arg, Lys or His

<220>
<221> MOD_RES
<222> (100)
<223> Arg, His or Lys

<220>
<221> MOD_RES
<222> (107)
<223> Trp, Phe, Tyr, Arg, His or Lys

<220>
<221> MOD_RES
<222> (114)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr or Phe

<220>

<221> MOD_RES

<222> (115)

<223> Gln, Asn, Asp or Glu

<220>

<221> MOD_RES

<222> (116)

<223> Asp or Glu

<220>

<221> MOD_RES

<222> (125)

<223> Gly, Ala, Val, Leu, or Ile

<220>

<221> MOD_RES

<222> (134)

<223> Arg, His or Lys

<220>

<221> MOD_RES

<222> (135)

<223> Asn, Gln, Thr or Ser

<220>

<221> MOD_RES

<222> (139)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr, Met or Cys

<220>

<221> MOD_RES

<222> (141)

<223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>

<221> MOD_RES

<222> (157)

<223> Arg, His or Lys

<220>

<221> MOD_RES

<222> (158)

<223> Asn, Gln, Gly, Ala, Val, Leu or Ile

<220>

<221> MOD_RES

<222> (160)

<223> Gly, Ala, Val, Leu or Ile

<220>

<221> MOD_RES

<222> (162)

<223> Gly, Ala, Val, Leu, Ile, Ser, Thr or Cys

<220>

<221> MOD_RES
 <222> (166)
 <223> Gly, Ala, Val, Leu, Ile, Thr or Ser

<220>
 <221> MOD_RES
 <222> (167)
 <223> Asp or Glu

<220>
 <223> each Xaa may also be any amino acid.

<400> 22
 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
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Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
 35 40 45

Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 50 55 60

Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 85 90 95

Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 100 105 110

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
 130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa
 145 150 155 160

His Xaa Ser Val Lys Xaa Xaa
 165

<210> 23
 <211> 627
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(624)

<400> 23

atg tgg aaa tgg ata ctg aca cat tgt gcc tca gcc ttt ccc cac ctg Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu	48
1 5 10 15	
ccc ggc tgc tgc tgc tgc ttt ttg ttg ctg ttc ttg gtg tct tcc Pro Gly Cys Cys Cys Cys Phe Leu Leu Leu Phe Leu Val Ser Ser	96
20 25 30	
gtc cct gtc acc tgc caa gcc ctt ggt cag gac atg gtg tca cca gag Val Pro Val Thr Cys Gln Ala Leu Gly Gln Asp Met Val Ser Pro Glu	144
35 40 45	
gcc acc aac tct tct tcc tcc ttc tcc tct cct tcc agc gcg gga Ala Thr Asn Ser Ser Ser Ser Phe Ser Ser Pro Ser Ser Ala Gly	192
50 55 60	
agg cat gtg cgg agc tac aat cac ctt caa gga gat gtc cgc tgg aga Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg	240
65 70 75 80	
aag cta ttc tct ttc acc aag tac ttt ctc aag att gag aag aac ggg Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly	288
85 90 95	
aag gtc agc ggg acc aag aag gag aac tgc ccg tac agc atc ctg gag Lys Val Ser Gly Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu	336
100 105 110	
ata aca tca gta gaa atc gga gtt gtt gcc gtc aaa gcc att aac agc Ile Thr Ser Val Glu Ile Gly Val Val Ala Val Lys Ala Ile Asn Ser	384
115 120 125	
aac tat tac tta gcc atg aac aag aag ggg aaa ctc tat ggc tca aaa Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu Tyr Gly Ser Lys	432
130 135 140	
gaa ttt aac aat gac tgt aag ctg aag gag agg ata gag gaa aat gga Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly	480
145 150 155 160	
tac aat acc tat gca tca ttt aac tgg cag cat aat ggg agg caa atg Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met	528
165 170 175	
tat gtg gca ttg aat gga aaa gga gct cca agg aga gga cag aaa aca Tyr Val Ala Leu Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr	576
180 185 190	
cga agg aaa aac acc tct gct cac ttt ctt cca atg gtg gta cac tca Arg Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	624
195 200 205	
tag	627

<210> 24
<211> 208

<212> PRT

<213> Homo sapiens

<400> 24

Met	Trp	Lys	Trp	Ile	Leu	Thr	His	Cys	Ala	Ser	Ala	Phe	Pro	His	Leu
1				5				10						15	

Pro	Gly	Cys	Cys	Cys	Cys	Cys	Phe	Leu	Leu	Leu	Phe	Leu	Val	Ser	Ser
							20		25			30			

Val	Pro	Val	Thr	Cys	Gln	Ala	Leu	Gly	Gln	Asp	Met	Val	Ser	Pro	Glut
				35				40			45				

Ala	Thr	Asn	Ser	Ser	Ser	Ser	Phe	Ser	Ser	Pro	Ser	Ser	Ala	Gly
				50		55			60					

Arg	His	Val	Arg	Ser	Tyr	Asn	His	Leu	Gln	Gly	Asp	Val	Arg	Trp	Arg
	65				70				75			80			

Lys	Leu	Phe	Ser	Phe	Thr	Lys	Tyr	Phe	Leu	Lys	Ile	Glu	Lys	Asn	Gly
				85					90			95			

Lys	Val	Ser	Gly	Thr	Lys	Lys	Glu	Asn	Cys	Pro	Tyr	Ser	Ile	Leu	Glu
				100			105					110			

Ile	Thr	Ser	Val	Glu	Ile	Gly	Val	Val	Ala	Val	Lys	Ala	Ile	Asn	Ser
				115			120				125				

Asn	Tyr	Tyr	Leu	Ala	Met	Asn	Lys	Lys	Gly	Lys	Leu	Tyr	Gly	Ser	Lys
		130				135			140						

Glu	Phe	Asn	Asn	Asp	Cys	Lys	Leu	Lys	Glu	Arg	Ile	Glu	Glu	Asn	Gly
145					150				155			160			

Tyr	Asn	Thr	Tyr	Ala	Ser	Phe	Asn	Trp	Gln	His	Asn	Gly	Arg	Gln	Met
			165					170			175				

Tyr	Val	Ala	Leu	Asn	Gly	Lys	Gly	Ala	Pro	Arg	Arg	Gly	Gln	Lys	Thr
			180				185			190					

Arg	Arg	Lys	Asn	Thr	Ser	Ala	His	Phe	Leu	Pro	Met	Val	Val	His	Ser
		195				200				205					

<210> 25

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

gcgcgcgttcg aagcgaggca gccagcgagg gagagagcga gccccggcggc 60

aaatcgatgc gcgc

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<210> 26
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 26
gcgcgcagat ctgggaaagc gcaagagaga gcgcacacgc acacacccgc cgcgcgact 60
cggatccgc gcgc                                         74

<210> 27
<211> 996
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: gene
      activation construct

<400> 27
cgaagcgagg cagccagcga gggagagagc gagcgggcga gccggagcga ggaaatcgaa 60
gttcgaatc cttcccccac caccatcact ttcaaaaagtc cgaaagaatc tgctccctgc 120
ttgtgttgtg gaggtcgctg agtagtgcgc gagtaaaatt taagctacaa caaggcaagg 180
cttgaccgac aattgcatga agaatctgct tagggttagg cgtttgcgc tgcttcgcga 240
tgtacgggcc agatatacgc gttgacattt attattgact agttattaat agtaatcaat 300
tacggggtca ttagttcata gcccataat ggagttccgc gttacataac ttacggtaaa 360
tggcccgct ggctgaccgc ccaacgaccc ccgeccattt acgtcaataa tgacgtatgt 420
tcccatagta acgccaatag ggactttcca ttgacgtcaa tgggtggact atttacggta 480
aactgcccac ttggcagtac atcaagtgtt tcatatgcca agtacgcccc ctattgacgt 540
caatgacggt aaatggcccg cctggcatta tgcccagtac atgaccttat gggactttcc 600
tacttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggaaaaatggca 660
gtacatcaat gggcgtggat agcggttga ctcacggggta tttccaagtc tccacccat 720
tgacgtcaat gggagttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 780
caactccgccc ccattgacgc aaatggccgg taggcgtgtt cgggtggagg tctatataag 840
cagagctctc tggctaacta gagaaccac tgcttactgg cttatcgaaa ttaatacgac 900
tcactatagg gagacccaag cttggtacgg agctcgatc gatctggaa agcgcaagag 960
agagcgcaca cgcacacacc cggccgcgc actcgg                                         996

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<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense construct

<400> 28
gtcctggcg cgcgcgccc gtcgcc

26

<210> 29
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense construct

<400> 29
ttccgatgac cggccttgc cggtga

26

B /
Cmt

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: antisense construct

<400> 30
gtgcacggaa aggtgcaggg cacact

26